

SEQUENCE LISTING

<110> Max-Planck-Gesellschaft zur Foerderung der Wissens

<120> Human semaphorin 6A-1 (SEMA6A-1), a novel gene involved
in neuronal development and regeneration mechanisms
during apoptosis, as a potential drug target structure

<130> 19592

<140>

<141>

<150> 98122441.3

<151> 1998-11-26

<160> 7

<170> PatentIn Ver. 2.1

<210> 1

<211> 3093

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(3093)

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Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr				
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Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys				
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His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn				
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Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys				
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aga aac tat aag atg gat aca ttg gaa cca ttc ggg gat gaa ttc agc				480
Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser				
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Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu				
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Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala				
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Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg				
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Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln				
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Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln				
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Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln				

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Cys	Ala	Gly	Ser	Ser	Ser	Leu	Glu	Arg	Tyr	Ala	Thr	Ser	Asn	Glu	Phe				
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cct	gat	gat	acc	ctg	aac	ttc	atc	aag	acg	cac	ccg	ctc	atg	gat	gag	1200			
Pro	Asp	Asp	Thr	Leu	Asn	Phe	Ile	Lys	Thr	His	Pro	Leu	Met	Asp	Glu				
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Arg	Tyr	Arg	Leu	Thr	Lys	Ile	Ala	Val	Asp	Thr	Ala	Ala	Gly	Pro	Tyr				
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Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp			
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gga gtc gaa gac aaa agg atc atg ggc atg cag ctg gac aga gca agc			1488
Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser			
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Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu			
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Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser			
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Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His			
530	535	540	
tta tca ccc aac agc aga ctg act ttt gag cag gac ata gag cgt ggc			1680
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aat aca gat ggt ctg ggg gac tgt cac aat tcc ttt gtg gca ctg aat			1728
Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn			
565	570	575	
ggg cat tcc agt tcc ctc ttg ccc agc aca acc aca tca gat tgc acg			1776
Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr			
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Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His			
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Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser			
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His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys			
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ggc cac gac cag ctg gtt ccc gtc acc ctc ttg gcc att gca gtc atc			1968
Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala Val Ile			

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Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val Tyr Cys			
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gtc tgt gat cat cgg cgc aaa gac gtg gct gtg gtg cag cgc aag gag			2064
Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu			
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aag gag ctc acc cac tcg cgc cgg ggc tcc atg agc agc gtc acc aag			2112
Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys			
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ctc agc ggc ctc ttt ggg gac act caa tcc aaa gac cca aag ccg gag			2160
Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys Pro Glu			
705	710	715	720
gcc atc ctc acg cca ctc atg cac aac ggc aag ctc gcc act ccc ggc			2208
Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly			
725	730	735	
aac acg gcc aag atg ctc att aaa gca gac cag cac cac ctg gac ctg			2256
Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu Asp Leu			
740	745	750	
acg gcc ctc ccc acc cca gag tca acc cca acg ctg cag cag aag cgg			2304
Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln Lys Arg			
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aag ccc agc cgc ggc agc cgc gag tgg gag agg aac cag aac ctc atc			2352
Lys Pro Ser Arg Gly Ser Arg Glu Trp Glu Arg Asn Gln Asn Leu Ile			
770	775	780	
aat gcc tgc aca aag gac atg ccc ccc atg ggc tcc cct gtg att ccc			2400
Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val Ile Pro			
785	790	795	800
acg gac ctg ccc ctg cgg gcc tcc ccc agc cac atc ccc agc gtg gtg			2448
Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser Val Val			
805	810	815	
gtc ctg ccc atc acg cag cag ggc tac cag cat gag tac gtg gac cag			2496
Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val Asp Gln			
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[illegible]

- 17 -

1025

1030

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<211> 1030

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Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
 35 40 45

Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
 50 55 60

Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
 65 70 75 80

Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
 85 90 95

Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
 100 105 110

His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
 115 120 125

Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys
 130 135 140

Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser
 145 150 155 160

Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu
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Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala
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Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg
 195 200 205

0955651.050301
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Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln
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Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala
 225 230 235 240

Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln
 245 250 255

Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln
 260 265 270

Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
 275 280 285

Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg
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Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn
 305 310 315 320

Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala
 325 330 335

Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr
 340 345 350

Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys
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Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe
 370 375 380

Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu
 385 390 395 400

Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val
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Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr
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Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu
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Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
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Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser
485 490 495

Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu
500 505 510

Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser
515 520 525

Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
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Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly
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Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn
565 570 575

Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr
580 585 590

Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His
595 600 605

Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser
610 615 620

His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys
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Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala Val Ile
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Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val Tyr Cys
660 665 670

Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu
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Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys
690 695 700

Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys Pro Glu
705 710 715 720

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Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly
725 730 735

Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu Asp Leu
740 745 750

Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln Lys Arg
755 760 765

Lys Pro Ser Arg Gly Ser Arg Glu Trp Glu Arg Asn Gln Asn Leu Ile
770 775 780

Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val Ile Pro
785 790 795 800

Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser Val Val
805 810 815

Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val Asp Gln
820 825 830

Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln Ala Ala
835 840 845

Thr Leu Glu Tyr Lys Thr Ile Lys Glu His Leu Ser Ser Lys Ser Pro
850 855 860

Asn His Gly Val Asn Leu Val Glu Asn Leu Asp Ser Leu Pro Pro Lys
865 870 875 880

Val Pro Gln Arg Glu Ala Ser Leu Gly Pro Pro Gly Ala Ser Leu Ser
885 890 895

Gln Thr Gly Leu Ser Lys Arg Leu Glu Met His His Ser Ser Ser Tyr
900 905 910

Gly Val Asp Tyr Lys Arg Ser Tyr Pro Thr Asn Ser Leu Thr Arg Ser
915 920 925

His Gln Ala Thr Thr Leu Lys Arg Asn Asn Thr Asn Ser Ser Asn Ser
930 935 940

Ser His Leu Ser Arg Asn Gln Ser Phe Gly Arg Gly Asp Asn Pro Pro
945 950 955 960

Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser Gln Pro
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Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu Lys Pro
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<222> (1)..(216)

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 Gln Pro Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn
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gcc tac aac tca ctg aca agg tcg ggg ctg aag cgt acg ccc tcg cta 144
 Ala Tyr Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu
 35 40 45

aag ccg gac gta ccc ccc aaa cca tcc ttt gct ccc ctt tcc aca tcc 192
 Lys Pro Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser
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 Met Lys Pro Asn Asp Ala Cys Thr
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<213> Homo sapiens

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 20 25 30

Ala Tyr Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu
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Lys Pro Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser
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Met Lys Pro Asn Asp Ala Cys Thr
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<213> Homo sapiens

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Pro Gln Ala Lys Pro His Val Gln Pro Gln Pro Val Ser Ser Ala Asn
 20 25 30

Thr Gln Pro Arg Gly Pro Leu Ser Gln Ala Pro Thr Pro Ala Pro Lys
 35 40 45

Phe Ala Pro Val Ala Pro Lys Phe Thr Pro Val Val Ser Lys Phe Ser
 50 55 60

Pro
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<222> (658)..(3750)

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 ggaatgacaa aggcttgca aggagagagc cgcagccgcg gcccgagag atccctcga 540
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 atg agg tca gaa gcc ttg ctg cta tat ttc aca ctg cta cac ttt gct 705
 Met Arg Ser Glu Ala Leu Leu Leu Tyr Phe Thr Leu Leu His Phe Ala
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 Gly Ala Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
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 aac tat aca aaa cag tat ccg gtg ttt gtg ggc cac aag cca gga cgg 801
 Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
 35 40 45
 aac acc aca cag agg cac agg ctg gac atc cag atg att atg atc atg 849
 Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
 50 55 60
 aac gga acc ctc tac att gct gct agg gac cat att tat act gtt gat 897
 Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
 65 70 75 80
 ata gac aca tca cac acg gaa gaa att tat tgt agc aaa aaa ctg aca 945

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Figure 1 consists of 11 sub-diagrams labeled (a) through (k), arranged vertically. Each diagram shows a cross-section of a vortex structure. The horizontal axis represents a spatial coordinate, and the vertical axis represents a physical quantity. The diagrams illustrate the temporal evolution of the vortex. (a) shows a single vortex with a central core and a surrounding ring. (b) through (j) show the vortex elongating and developing a secondary core. (k) shows the final state with two distinct cores. Each diagram includes numerical data points along the horizontal axis.

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Trp	Thr	Ser	Phe	Leu	Lys	Ala	Arg	Leu	Asn	Cys	Ser	Val	Pro	Gly	Asp	
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Ser	His	Phe	Tyr	Phe	Asn	Ile	Leu	Gln	Ala	Val	Thr	Asp	Val	Ile	Arg	
		290				295				300						
atc	aac	ggg	cgt	gat	gtt	gtc	ctg	gca	acg	ttt	tct	aca	cct	tat	aac	1617
Ile	Asn	Gly	Arg	Asp	Val	Val	Leu	Ala	Thr	Phe	Ser	Thr	Pro	Tyr	Asn	
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Ser	Ile	Pro	Gly	Ser	Ala	Val	Cys	Ala	Tyr	Asp	Met	Leu	Asp	Ile	Ala	
				325				330						335		
agt	gtt	ttt	act	ggg	aga	ttc	aag	gaa	cag	aag	tct	cct	gat	tcc	acc	1713
Ser	Val	Phe	Thr	Gly	Arg	Phe	Lys	Glu	Gln	Lys	Ser	Pro	Asp	Ser	Thr	
			340				345						350			
tgg	aca	cca	gtt	cct	gat	gaa	cga	gtt	cct	aag	ccc	agg	cca	ggg	tgc	1761
Trp	Thr	Pro	Val	Pro	Asp	Glu	Arg	Val	Pro	Lys	Pro	Arg	Pro	Gly	Cys	
		355				360					365					
tgt	gct	ggc	tca	tcc	tcc	tta	gaa	aga	tat	gca	acc	tcc	aat	gag	ttc	1809
Cys	Ala	Gly	Ser	Ser	Ser	Leu	Glu	Arg	Tyr	Ala	Thr	Ser	Asn	Glu	Phe	
	370					375				380						
cct	gat	gat	acc	ctg	aac	ttc	atc	aag	acg	cac	ccg	ctc	atg	gat	gag	1857
Pro	Asp	Asp	Thr	Leu	Asn	Phe	Ile	Lys	Thr	His	Pro	Leu	Met	Asp	Glu	
385					390				395					400		
gca	gtg	ccc	tcc	atc	ttc	aac	agg	cca	tgg	ttc	ctg	aga	aca	atg	gtc	1905
Ala	Val	Pro	Ser	Ile	Phe	Asn	Arg	Pro	Trp	Phe	Leu	Arg	Thr	Met	Val	
				405				410					415			
aga	tac	cgc	ctt	acc	aaa	att	gca	gtg	gac	aca	gct	gct	ggg	cca	tat	1953
Arg	Tyr	Arg	Leu	Thr	Lys	Ile	Ala	Val	Asp	Thr	Ala	Ala	Gly	Pro	Tyr	
			420					425					430			
cag	aat	cac	act	gtg	gtt	ttt	ctg	gga	tca	gag	aag	gga	atc	atc	ttg	2001
Gln	Asn	His	Thr	Val	Val	Phe	Leu	Gly	Ser	Glu	Lys	Gly	Ile	Ile	Leu	
		435				440						445				
aag	ttt	ttg	gcc	aga	ata	gga	aat	agt	ggt	ttt	cta	aat	gac	agc	ctt	2049
Lys	Phe	Leu	Ala	Arg	Ile	Gly	Asn	Ser	Gly	Phe	Leu	Asn	Asp	Ser	Leu	
		450				455					460					
ttc	ctg	gag	gag	atg	agt	gtt	tac	aac	tct	gaa	aaa	tgc	agc	tat	gat	2097

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Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp
 465 470 475 480

gga gtc gaa gac aaa agg atc atg ggc atg cag ctg gac aga gca agc 2145
 Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser
 485 490 495

agc tct ctg tat gtt gcg ttc tct acc tgt gtg ata aag gtt ccc ctt 2193
 Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu
 500 505 510

ggc cgg tgt gaa cga cat ggg aag tgt aaa aaa acc tgt att gcc tcc 2241
 Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser
 515 520 525

aga gac cca tat tgt gga tgg ata aag gaa ggt ggt gcc tgc agc cat 2289
 Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
 530 535 540

tta tca ccc aac agc aga ctg act ttt gag cag gac ata gag cgt ggc 2337
 Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly
 545 550 555 560

aat aca gat ggt ctg ggg gac tgt cac aat tcc ttt gtg gca ctg aat 2385
 Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn
 565 570 575

ggg cat tcc agt tcc ctc ttg ccc agc aca acc aca tca gat tcg acg 2433
 Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr
 580 585 590

gct caa gag ggg tat gag tct agg gga gga atg ctg gac tgg aag cat 2481
 Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His
 595 600 605

ctg ctt gac tca cct gac agc aca gac cct ttg ggg gca gtg tct tcc 2529
 Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser
 610 615 620

cat aat cac caa gac aag aag gga gtg att cgg gaa agt tac ctc aaa 2577
 His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys
 625 630 635 640

ggc cac gac cag ctg gtt ccc gtc acc ctc ttg gcc att gca gtc atc 2625
 Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala Val Ile
 645 650 655

ctg gct ttc gtc atg ggg gcc gtc ttc tcg ggc atc acc gtc tac tgc 2673

Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val Tyr Cys
 660 665 670

gtc tgt gat cat cgg cgc aaa gac gtg gct gtg gtg cag cgc aag gag 2721
 Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu
 675 680 685

aag gag ctc acc cac tcg cgc cgg ggc tcc atg agc agc gtc acc aag 2769
 Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys
 690 695 700

ctc agc ggc ctc ttt ggg gac act caa tcc aaa gac cca aag ccg gag 2817
 Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys Pro Glu
 705 710 715 720

gcc atc ctc acg cca ctc atg cac aac ggc aag ctc gcc act ccc ggc 2865
 Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly
 725 730 735

aac acg gcc aag atg ctc att aaa gca gac cag cac cac ctg gac ctg 2913
 Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu Asp Leu
 740 745 750

acg gcc ctc ccc acc cca gag tca acc cca acg ctg cag cag aag cgg 2961
 Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Lys Arg
 755 760 765

aag ccc agc cgc ggc agc cgc gag tgg gag agg aac cag aac ctc atc 3009
 Lys Pro Ser Arg Gly Ser Arg Glu Trp Glu Arg Asn Gln Asn Leu Ile
 770 775 780

aat gcc tgc aca aag gac atg ccc ccc atg ggc tcc cct gtg att ccc 3057
 Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val Ile Pro
 785 790 795 800

acg gac ctg ccc ctg cgg gcc tcc ccc agc cac atc ccc agc gtg gtg 3105
 Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser Val Val
 805 810 815

gtc ctg ccc atc acg cag cag ggc tac cag cat gag tac gtg gac cag 3153
 Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val Asp Gln
 820 825 830

ccc aaa atg agc gag gtg gcc cag atg gcg ctg gag gac cag gcc gcc 3201
 Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln Ala Ala
 835 840 845

aca ctg gag tat aag acc atc aag gaa cat ctc agc agc aag agt ccc 3249

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Thr Leu Glu Tyr Lys Thr Ile Lys Glu His Leu Ser Ser Lys Ser Pro
 850 855 860

aac cat ggg gtg aac ctt gtg gag aac ctg gac agc ctg ccc ccc aaa 3297
 Asn His Gly Val Asn Leu Val Glu Asn Leu Asp Ser Leu Pro Pro Lys
 865 870 875 880

gtt cca cag cgg gag gcc tcc ctg ggt ccc ccg gga gcc tcc ctg tct 3345
 Val Pro Gln Arg Glu Ala Ser Leu Gly Pro Pro Gly Ala Ser Leu Ser
 885 890 895

cag acc ggt cta agc aag cgg ctg gaa atg cac cac tcc tct tcc tac 3393
 Gln Thr Gly Leu Ser Lys Arg Leu Glu Met His His Ser Ser Ser Tyr
 900 905 910

ggg gtt gac tat aag agg agc tac ccc acg aac tcg ctc acg aga agc 3441
 Gly Val Asp Tyr Lys Arg Ser Tyr Pro Thr Asn Ser Leu Thr Arg Ser
 915 920 925

cac cag gcc acc act ctc aaa aga aac aac act aac tcc tcc aat tcc 3489
 His Gln Ala Thr Thr Leu Lys Arg Asn Asn Thr Asn Ser Ser Asn Ser
 930 935 940

tct cac ctc tcc aga aac cag agc ttt ggc agg gga gac aac ccg ccg 3537
 Ser His Leu Ser Arg Asn Gln Ser Phe Gly Arg Gly Asp Asn Pro Pro
 945 950 955 960

ccc gcc ccg cag agg gtg gac tcc atc cag gtg cac agc tcc cag cca 3585
 Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser Gln Pro
 965 970 975

tct ggc cag gcc gtg act gtc tcg agg cag ccc agc ctc aac gcc tac 3633
 Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn Ala Tyr
 980 985 990

aac tca ctg aca agg tcg ggg ctg aag cgt acg ccc tcg cta aag ccg 3681
 Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu Lys Pro
 995 1000 1005

gac gta ccc ccc aaa cca tcc ttt gct ccc ctt tcc aca tcc atg aag 3729
 Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser Met Lys
 1010 1015 1020

ccc aat gat gcg tgt aca taa tcccaggggg aggggggtcag gtgtcgaacc 3780
 Pro Asn Asp Ala Cys Thr
 1025 1030

agcaggcaag gcgaggtgcc cgctcagctc agcaagggttc tcaactgcct cgagtaccca 3840

ccagaccaag aaggcctgcg gc

38 62

<400> 7
Met Arg Ser Glu Ala Leu Leu Leu Tyr Phe Thr Leu Leu His Phe Ala

1 5 10 15

Gly Ala Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
20 25 30

Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
35 40 45

Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
50 55 60

Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
65 70 75 80

Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
85 90 95

Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
100 105 110

His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
115 120 125

Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys
130 135 140

Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser
145 150 155 160

Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu
165 170 175

Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala
180 185 190

Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg
195 200 205

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Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
450 455 460

[illegible]

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Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp
 465 470 475 480

Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser
 485 490 495

Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu
 500 505 510

Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser
 515 520 525

Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
 530 535 540

Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly
 545 550 555 560

Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn
 565 570 575

Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr
 580 585 590

Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His
 595 600 605

Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser
 610 615 620

His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys
 625 630 635 640

Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala Val Ile
 645 650 655

Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val Tyr Cys
 660 665 670

Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu
 675 680 685

Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys
 690 695 700

Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys Pro Glu
 705 710 715 720

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Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly
725 730 735

Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu Asp Leu
740 745 750

Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln Lys Arg
755 760 765

Lys Pro Ser Arg Gly Ser Arg Glu Trp Glu Arg Asn Gln Asn Leu Ile
770 775 780

Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val Ile Pro
785 790 795 800

Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser Val Val
805 810 815

Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val Asp Gln
820 825 830

Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln Ala Ala
835 840 845

Thr Leu Glu Tyr Lys Thr Ile Lys Glu His Leu Ser Ser Lys Ser Pro
850 855 860

Asn His Gly Val Asn Leu Val Glu Asn Leu Asp Ser Leu Pro Pro Lys
865 870 875 880

Val	Pro	Gln	Arg	Glu	Ala	Ser	Leu	Gly	Pro	Pro	Gly	Ala	Ser	Leu	Ser
				885				890						895	

Gln Thr Gly Leu Ser Lys Arg Leu Glu Met His His Ser Ser Ser Tyr
900 905 910

Gly Val Asp Tyr Lys Arg Ser Tyr Pro Thr Asn Ser Leu Thr Arg Ser
915 920 925

His Gln Ala Thr Thr Leu Lys Arg Asn Asn Thr Asn Ser Ser Asn Ser
930 935 940

Ser His Leu Ser Arg Asn Gln Ser Phe Gly Arg Gly Asp Asn Pro Pro
945 950 955 960

Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser Gln Pro
965 970 975

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Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn Ala Tyr
980 985 990

Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu Lys Pro
995 1000 1005

Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser Met Lys
1010 1015 1020

Pro Asn Asp Ala Cys Thr
025 1030

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100